

ATTORNEY DOCKET NO. 21108.0034P1

SEQUENCE LISTING

<110> Univ. of Rochester

SMITH, Harold
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 KIM, Baek
 WEDEKIND, Joseph

<120> PROTEIN TRANSDUCING DOMAIN/DEAMINASE
 CHIMERIC PROTEINS, RELATED COMPOUNDS, AND USES THEREOF

<130> 21108.0034P1

<140> Unassigned

<141> 2003-08-05

<150> 60/419,982

<151> 2002-10-21

<150> 60/401,293

<151> 2002-08-05

<160> 49

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 384

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 1

Met	Lys	Pro	His	Phe	Arg	Asn	Thr	Val	Glu	Arg	Met	Tyr	Arg	Asp	Thr
1				5					10					15	
Phe	Ser	Tyr	Asn	Phe	Tyr	Asn	Arg	Pro	Ile	Leu	Ser	Arg	Arg	Asn	Thr
			20					25					30		
Val	Trp	Leu	Cys	Tyr	Glu	Val	Lys	Thr	Lys	Gly	Pro	Ser	Arg	Pro	Pro
		35					40					45			
Leu	Asp	Ala	Lys	Ile	Phe	Arg	Gly	Gln	Val	Tyr	Ser	Glu	Leu	Lys	Tyr
	50				55					60					
His	Pro	Glu	Met	Arg	Phe	Phe	His	Trp	Phe	Ser	Lys	Trp	Arg	Lys	Leu
	65				70				75					80	
His	Arg	Asp	Gln	Glu	Tyr	Glu	Val	Thr	Trp	Tyr	Ile	Ser	Trp	Ser	Pro
			85					90					95		
Cys	Thr	Lys	Cys	Thr	Arg	Asp	Met	Ala	Thr	Phe	Leu	Ala	Glu	Asp	Pro
			100				105						110		
Lys	Val	Thr	Leu	Thr	Ile	Phe	Val	Ala	Arg	Leu	Tyr	Tyr	Phe	Trp	Asp
			115				120					125			

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Pro Asp Tyr Gln Glu Ala Leu Arg Ser Leu Cys Gln Lys Arg Asp Gly
 130 135 140
 Pro Arg Ala Thr Met Lys Ile Met Asn Tyr Asp Glu Phe Gln His Cys
 145 150 155 160
 Trp Ser Lys Phe Val Tyr Ser Gln Arg Glu Leu Phe Glu Pro Trp Asn
 165 170 175
 Asn Leu Pro Lys Tyr Tyr Ile Leu Leu His Ile Met Leu Gly Glu Ile
 180 185 190
 Leu Arg His Ser Met Asp Pro Pro Thr Phe Thr Phe Asn Phe Asn Asn
 195 200 205
 Glu Pro Trp Val Arg Gly Arg His Glu Thr Tyr Leu Cys Tyr Glu Val
 210 215 220
 Glu Arg Met His Asn Asp Thr Trp Val Leu Leu Asn Gln Arg Arg Gly
 225 230 235 240
 Phe Leu Cys Asn Gln Ala Pro His Lys His Gly Phe Leu Glu Gly Arg
 245 250 255
 His Ala Glu Leu Cys Phe Leu Asp Val Ile Pro Phe Trp Lys Leu Asp
 260 265 270
 Leu Asp Gln Asp Tyr Arg Val Thr Cys Phe Thr Ser Trp Ser Pro Cys
 275 280 285
 Phe Ser Cys Ala Gln Glu Met Ala Lys Phe Ile Ser Lys Asn Lys His
 290 295 300
 Val Ser Leu Cys Ile Phe Thr Ala Arg Ile Tyr Asp Asp Gln Gly Arg
 305 310 315 320
 Cys Gln Glu Gly Leu Arg Thr Leu Ala Glu Ala Gly Ala Lys Ile Ser
 325 330 335
 Ile Met Thr Tyr Ser Glu Phe Lys His Cys Trp Asp Thr Phe Val Asp
 340 345 350
 His Gln Gly Cys Pro Phe Gln Pro Trp Asp Gly Leu Asp Glu His Ser
 355 360 365
 Gln Asp Leu Ser Gly Arg Leu Arg Ala Ile Leu Gln Asn Gln Glu Asn
 370 375 380

<210> 2

<211> 1155

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

atgaagcctc	acttcagaaa	cacagtggag	cgaatgtatc	gagacacatt	ctcctacaac	60
ttttataata	gacccatcct	ttctcgtcgg	aataccgtct	ggctgtgcta	cgaagtgaac	120
acaaagggtc	cctcaaggcc	ccctttggac	gcaaagatct	ttcgaggcca	ggtgtattcc	180
gaacttaagt	accaccaga	gatgagattc	ttccactgg	tcagcaagt	gaggaagctg	240
catcgtgacc	aggagtatga	ggtcacctgg	tacatatcct	ggagcccctg	cacaaagtgt	300
acaagggata	tggccacgtt	cctggccgag	gacccgaagg	ttaccctgac	catcttcgtt	360
gcccgcctct	actacttctg	ggaccagat	taccaggagg	cgcttcgcag	cctgtgtcag	420
aaaagagacg	gtccgcgtgc	caccatgaag	atcatgaatt	atgacgaatt	tcagcactgt	480
tggagcaagt	tcgtgtacag	ccaaagagag	ctatttgagc	cttggaataa	tctgcctaaa	540
tattatatat	tactgcacat	catgctgggg	gagattctca	gacactcgat	ggatccaccc	600
acattcactt	tcaactttaa	caatgaacct	tgggtcagag	gacggcatga	gacttacctg	660
tgttatgagg	tggagcgcat	gcacaatgac	acctgggtcc	tgctgaacca	gcgcaggggc	720
tttctatgca	accaggctcc	acataaacac	ggtttccttg	aaggccgcca	tcgagagctg	780

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tgcttcctgg acgtgattcc cttttggaag ctggacctgg accaggacta cagggttacc      840
tgcttcacct cctggagccc ctgcttcagc tgtgcccagg aaatggctaa attcatttca      900
aaaaacaaac acgtgagcct gtgcatcttc actgcccgca tctatgatga tcaaggaaga      960
tgtcaggagg ggtgcgcac cctggccgag gctggggcca aaatttcaat aatgacatac     1020
agtgaattta agcactgctg ggacaccttt gtggaccacc agggatgtcc cttccagccc     1080
tgggatggac tagatgagca cagccaagac ctgagtggga ggctgcgggc cattctccag     1140
aatcaggaaa actga                                     1155

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<210> 3
 <211> 198
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 3
Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
 1           5           10           15
Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
 20           25           30
Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
 35           40           45
Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
 50           55           60
Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
 65           70           75           80
Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
 85           90           95
Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg
 100          105          110
Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
 115          120          125
Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
 130          135          140
Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
 145          150          155          160
Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
 165          170          175
Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
 180          185          190
Phe Arg Thr Leu Gly Leu
 195

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<210> 4
 <211> 597
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 4
atggacagcc tcttgatgaa ccggaggaag tttctttacc aattcaaaaa tgtccgctgg      60

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gctaagggtc ggcgtagac ctacctgtgc tacgtagtga agaggcgtga cagtgtctaca 120
tcctttttcac tggactttgg ttatcttcgc aataagaacg gctgccacgt ggaattgctc 180
ttcctccgct acatctcggg ctggggacct gaccctggcc gctgtaccg cgtcacctgg 240
ttcacctcct ggagcccctg ctacgactgt gcccgcacatg tggccgactt tctgcgaggg 300
aaccccaacc tcagtctgag gatcttcacc gcgcgcctct acttctgtga ggaccgcaag 360
gctgagcccg aggggctgcg gcggctgcac cgcgccgggg tgcaaatagc catcatgacc 420
ttcaaagatt atttttactg ctggaatact tttgtagaaa accatgaaag aactttcaaa 480
gcctgggaag ggctgcatga aaattcagtt cgtctctcca gacagcttcg gcgcacacct 540
ttgccctgtg atgaggttga tgacttacga gacgcatttc gtactttggg actttga 597

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<210> 5

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5

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Met Thr Ser Glu Lys Gly Pro Ser Thr Gly Asp Pro Thr Leu Arg Arg
1          5          10          15
Arg Ile Glu Pro Trp Glu Phe Asp Val Phe Tyr Asp Pro Arg Glu Leu
20          25          30
Arg Lys Glu Ala Cys Leu Leu Tyr Glu Ile Lys Trp Gly Met Ser Arg
35          40          45
Lys Ile Trp Arg Ser Ser Gly Lys Asn Thr Thr Asn His Val Glu Val
50          55          60
Asn Phe Ile Lys Lys Phe Thr Ser Glu Arg Asp Phe His Pro Ser Ile
65          70          75          80
Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Trp Glu Cys
85          90          95
Ser Gln Ala Ile Arg Glu Phe Leu Ser Arg His Pro Gly Val Thr Leu
100         105         110
Val Ile Tyr Val Ala Arg Leu Phe Trp His Met Asp Gln Gln Asn Arg
115         120         125
Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln Ile Met
130         135         140
Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe Val Asn Tyr Pro
145         150         155         160
Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro Leu Trp Met Met
165         170         175
Leu Tyr Ala Leu Glu Leu His Cys Ile Ile Leu Ser Leu Pro Pro Cys
180         185         190
Leu Lys Ile Ser Arg Arg Trp Gln Asn His Leu Thr Phe Phe Arg Leu
195         200         205
His Leu Gln Asn Cys His Tyr Gln Thr Ile Pro Pro His Ile Leu Leu
210         215         220
Ala Thr Gly Leu Ile His Pro Ser Val Ala Trp Arg
225         230         235

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<210> 6

<211> 863

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 6

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gaaccctggg	agtttgacgt	cttctatgac	cccagagaac	ttcgtaaaga	ggcctgtctg	120
ctctacgaaa	tcaagtgggg	catgagccgg	aagatctggc	gaagctcagg	caaaaacacc	180
accaatcacg	tggaagttaa	ttttataaaa	aaatttacgt	cagaaagaga	ttttcaccca	240
tccatcagct	gctccatcac	ctggttcttg	tcctggagtc	cctgctggga	atgctcccag	300
gctattagag	agttttctgag	tcggcaccct	ggtgtgactc	tagtgatcta	cgtagctcgg	360
cttttttggc	acatggatca	acaaaatcgg	caaggtctca	gggaccttgt	taacagtgga	420
gtaactattc	agattatgag	agcatcagag	tattatcact	gctggaggaa	ttttgtcaac	480
taccacactg	gggatgaagc	tcactggcca	caatacccac	ctctgtggat	gatgtgttac	540
gcactggagc	tgcaactgat	aattctaagt	cttccaccct	gtttaaagat	ttcaagaaga	600
tggaacaaatc	atcttacatt	tttcagactt	catcttcaaa	actgccatta	ccaaacgatt	660
ccgccacaca	tccttttagc	tacagggctg	atacatcctt	ctgtggcttg	gagatgaata	720
ggatgattcc	gtgtgtgtac	tgattcaaga	acaagcaatg	atgaccact	aaagagtga	780
tgccatttag	aatctagaaa	tgttcacaag	gtaccccaaa	actctgtagc	ttaaaccaac	840
aataaatatg	tattacctct	ggc				863

<210> 7

<211> 192

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 7

Met	Glu	Asn	Arg	Trp	Gln	Val	Met	Ile	Val	Trp	Gln	Val	Asp	Arg	Met	15
1				5					10							
Arg	Ile	Lys	Thr	Trp	Lys	Ser	Leu	Val	Lys	His	His	Met	Tyr	Ile	Ser	30
			20					25								
Lys	Lys	Ala	Lys	Glu	Trp	Val	Tyr	Arg	His	His	Tyr	Glu	Ser	Thr	His	45
		35					40									
Pro	Arg	Ile	Ser	Ser	Glu	Val	His	Ile	Pro	Leu	Gly	Asp	Ala	Lys	Leu	60
		50				55										
Val	Ile	Thr	Thr	Tyr	Trp	Gly	Leu	His	Thr	Gly	Glu	Arg	Glu	Trp	His	80
65					70				75							
Leu	Gly	Gln	Gly	Val	Ser	Ile	Glu	Trp	Arg	Lys	Lys	Arg	Tyr	Asn	Thr	95
				85					90							
Gln	Val	Asp	Pro	Asp	Leu	Ala	Asp	Lys	Leu	Ile	His	Leu	His	Tyr	Phe	110
			100					105								
Asp	Cys	Phe	Ser	Asp	Ser	Ala	Ile	Arg	His	Ala	Ile	Leu	Gly	His	Arg	125
		115				120										
Val	Arg	Pro	Lys	Cys	Glu	Tyr	Gln	Ala	Gly	His	Asn	Lys	Val	Gly	Ser	140
		130				135										
Leu	Gln	Tyr	Leu	Ala	Leu	Thr	Ala	Leu	Ile	Thr	Pro	Lys	Lys	Ile	Lys	160
145					150					155						
Pro	Pro	Leu	Pro	Ser	Val	Arg	Lys	Leu	Thr	Glu	Asp	Arg	Trp	Asn	Lys	175
				165					170							
Pro	Gln	Lys	Thr	Lys	Gly	His	Arg	Gly	Ser	His	Thr	Met	Asn	Gly	His	190
			180					185								

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<210> 8
 <211> 569
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 8
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 tagtaaaaca ccatatgtat atttcaaaga aagctaagga atgggtctat agacatcact 120
 atgaaagcac tcatccaaga ataagttcag aagtacacat ccactaggg gatgctaaat 180
 tagtaataac aacatattgg ggtctgcata caggagaaag agaatggcat ctgggtcagg 240
 gagtctccat agaatggagg aaaaagagat ataatacaca agtagaccct gacctagcag 300
 acaaaactaat ccacctgcat tattttgatt gtttttcaga ctctgctata agacatgcca 360
 tattaggaca tagagttagg cctaagtgtg aatatcaagc aggacataac aaggtaggggt 420
 ctctacagta cttggcacta acagcattaa taacaccaa aaagataaag ccacctttgc 480
 ctagtgttag gaaactaaca gaggatagat ggaacaagcc ccagaagacc aaggggccaca 540
 gagggagcca tacaatgaat ggacactag 569

<210> 9
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 9
 Arg Gly Tyr Trp
 1

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 10
 cacttttaggg agggctgtcc 20

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 11
ctgtgatcag ctggagatgg 20

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 12
ctcccatggc aaagcctcac ttcagaaaca cag 33

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13
ctcctcgagg ttttctgat tctggagaat ggccc 35

<210> 14
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 14
Gln Gln Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr
1 5 10 15
Ile Gln Ile Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe
20 25 30
Val Asn Tyr Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro
35 40 45
Leu Trp Met
50

<210> 15
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

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<400> 15
 Pro Glu Thr Gln Gln Asn Leu Cys Arg Leu Val Gln Glu Gly Ala Gln
 1 5 10 15
 Val Ala Ala Met Asp Leu Tyr Glu Phe Lys Lys Cys Trp Lys Lys Phe
 20 25 30
 Val Asp Asn Gly Gly Arg Arg Phe Arg Pro Trp Lys Arg Leu Leu Thr
 35 40 45
 Asn Phe Arg
 50

<210> 16
 <211> 48
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 16
 Asp Gln Gln Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val
 1 5 10 15
 Thr Ile Gln Ile Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn
 20 25 30
 Phe Val Asn Tyr Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro
 35 40 45

<210> 17
 <211> 47
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 17
 Lys Arg-Pro Phe Gln Lys Gly Leu Cys Ser Leu Trp Gln Ser Gly Ile
 1 5 10 15
 Leu Val Asp Val Met Asp Leu Pro Gln Phe Thr Asp Cys Trp Thr Asn
 20 25 30
 Phe Val Asn Pro Lys Arg Pro Phe Trp Pro Trp Lys Gly Leu Glu
 35 40 45

<210> 18
 <211> 51
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 18
 Gln Gln Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr
 1 5 10 15
 Ile Gln Ile Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe
 20 25 30
 Val Asn Tyr Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro
 35 40 45
 Leu Trp Met
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<210> 19
 <211> 51
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 19
 Pro Glu Asn Gln Gln Asn Leu Cys Arg Leu Val Gln Glu Gly Ala Gln
 1 5 10 15
 Val Ala Ala Met Asp Leu Tyr Glu Phe Lys Lys Cys Trp Lys Lys Phe
 20 25 30
 Val Asp Asn Gly Gly Arg Arg Phe Arg Pro Trp Lys Lys Leu Leu Thr
 35 40 45
 Asn Phe Arg
 50

<210> 20
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 20
 Asn Arg Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln
 1 5 10 15
 Ile Met Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe Val Asn
 20 25 30
 Tyr Pro Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro
 35 40 45

<210> 21
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 21

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Phe Gln Lys Gly Leu Cys Ser Leu Trp Gln Ser Gly Ile Leu Val Asp
 1           5           10           15
Val Met Asp Leu Pro Gln Phe Thr Asp Cys Trp Thr Asn Phe Val Asn
          20           25           30
Pro Lys Arg Pro Phe Trp Pro Trp Lys Gly Leu Glu
      35           40

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<210> 22

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 22

aagtcaaaga aagaaagaca a

21

<210> 23

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 23

aagtcaaaga aagaaagaca a

21

<210> 24

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 24

ttcaggaagg agcccaggtg gctgccatgg acctatacg

39

<210> 25

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 25

ttcaggaagg agcccaggtg gctgccatgg acctatacg

39

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<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 26
tggtggacgt catggacctc ccac

24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 27
tggtggacgt catggacctc ccac

24

<210> 28
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 28
aatggccaag cgccactcaa aggctgcctg ctaagcgag

39

<210> 29
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 29
aatggccaag cgccactcaa aggctgcctg ctaagcgag

39

<210> 30
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

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<400> 30
aaaaaactgc ttacaaattt tagataccag gattctaagc ttcaggagat tctgag 56

<210> 31
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 31
aaaagactgc ttacaaattt tagataccag gattctaagc ttcaggagat tctgag 56

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 32
acaaaaggtc tccagagac gaggttctgc gtggagggca ggcgag 46

<210> 33
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 33
acaaaaggtc tccagagac gaggttctgg gtggagggca ggtgag 46

<210> 34
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 34
atgggaccat tctgtctggg atgcagccat cgcaaagtct attcaccgat cag 53

<210> 35
<211> 53
<212> DNA
<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 35

atgggaccat tctgtctggg atgcagccat cgcaaagtgt attcaccgat cag

53

<210> 36

<211> 4

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 36

ugau

4

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 37

ttacctgggt ctatggcagt

20

<210> 38

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 38

tgaaggctca gaatcccc

19

<210> 39

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 39

Met Arg Lys Lys Arg Arg Gln Arg Arg Arg Val Asp Ser Leu Leu Met
1 5 10 15

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Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys Asn Val Arg Trp Ala Lys
 20 25 30
 Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val Val Lys Arg Arg Asp Ser
 35 40 45
 Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr Leu Arg Asn Lys Asn Gly
 50 55 60
 Cys His Val Glu Leu Leu Phe Leu Arg Tyr Ile Ser Asp Trp Asp Leu
 65 70 75 80
 Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp Phe Thr Ser Trp Ser Pro
 85 90 95
 Cys Tyr Asp Cys Ala Arg His Val Ala Asp Phe Leu Arg Gly Asn Pro
 100 105 110
 Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg Leu Tyr Phe Cys Glu Asp
 115 120 125
 Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg Leu His Arg Ala Gly Val
 130 135 140
 Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr Phe Tyr Cys Trp Asn Thr
 145 150 155 160
 Phe Val Glu Asn His Glu Arg Thr Phe Lys Ala Trp Glu Gly Leu His
 165 170 175
 Glu Asn Ser Val Arg Leu Ser Arg Gln Leu Arg Arg Ile Leu Leu Pro
 180 185 190
 Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala Phe Arg Thr Leu Gly Leu
 195 200 205
 His Ala Ala Met Ala Asp Thr Phe Leu Glu His Met Cys Arg Leu Asp
 210 215 220
 Ile Asp Ser Glu Pro Thr Ile Ala Arg Asn Thr Gly Ile Ile Cys Thr
 225 230 235 240
 Ile Gly Pro Ala Ser Arg Ser Val Asp Lys Leu Lys Glu Met Ile Lys
 245 250 255
 Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr His Glu
 260 265 270
 Tyr His Glu Gly Thr Ile Lys Asn Val Arg Glu Ala Thr Glu Ser Phe
 275 280 285
 Ala Ser Asp Pro Ile Thr Tyr Arg Pro Val Ala Ile Ala Leu Asp Thr
 290 295 300
 Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly Thr Ala
 305 310 315 320
 Glu Val Glu Leu Lys Lys Gly Ala Ala Leu Lys Val Thr Leu Asp Asn
 325 330 335
 Ala Phe Met Glu Asn Cys Asp Glu Asn Val Leu Trp Val Asp Tyr Lys
 340 345 350
 Asn Leu Ile Lys Val Ile Asp Val Gly Ser Lys Ile Tyr Val Asp Asp
 355 360 365
 Gly Leu Ile Ser Leu Leu Val Lys Glu Lys Gly Lys Asp Phe Val Met
 370 375 380
 Thr Glu Val Glu Asn Gly Gly Met Leu Gly Ser Lys Lys Gly Val Asn
 385 390 395 400
 Leu Pro Gly Ala Ala Val Asp Leu Pro Ala Val Ser Glu Lys Asp Ile
 405 410 415
 Gln Asp Leu Lys Phe Gly Val Glu Gln Asn Val Asp Met Val Phe Ala
 420 425 430
 Ser Phe Ile Arg Lys Ala Ala Asp Val His Ala Val Arg Lys Val Leu
 435 440 445
 Gly Glu Lys Gly Lys His Ile Lys Ile Ile Ser Lys Ile Glu Asn His
 450 455 460

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Glu Gly Val Arg Arg Phe Asp Glu Ile Met Glu Ala Ser Asp Gly Ile
 465 470 475 480
 Met Val Ala Arg Gly Asp Leu Gly Ile Glu Ile Pro Ala Glu Lys Val
 485 490 495
 Phe Leu Ala Gln Lys Met Met Ile Gly Arg Cys Asn Arg Ala Gly Lys
 500 505 510
 Pro Ile Ile Cys Ala Thr Gln Met Leu Glu Ser Met Ile Lys Lys Pro
 515 520 525
 Arg Pro Thr Arg Ala Glu Gly Ser Asp Val Ala Asn Ala Val Leu Asp
 530 535 540
 Gly Ala Asp Cys Ile Met Leu Ser Gly Glu Thr Ala Lys Gly Asp Tyr
 545 550 555 560
 Pro Leu Glu Ala Val Arg Met Gln His Ala Ile Ala Arg Glu Ala Glu
 565 570 575
 Ala Ala Met Phe His Arg Gln Gln Phe Glu Glu Ile Leu Arg His Ser
 580 585 590
 Val His His Arg Glu Pro Ala Asp Ala Met Ala Ala Gly Ala Val Glu
 595 600 605
 Ala Ser Phe Lys Cys Leu Ala Ala Ala Leu Ile Val Met Thr Glu Ser
 610 615 620
 Gly Arg Ser Ala His Leu Val Ser Arg Tyr Arg Pro Arg Ala Pro Ile
 625 630 635 640
 Ile Ala Val Thr Arg Asn Asp Gln Thr Ala Arg Gln Ala His Leu Tyr
 645 650 655
 Arg Gly Val Phe Pro Val Leu Cys Lys Gln Pro Ala His Asp Ala Trp
 660 665 670
 Ala Glu Asp Val Asp Leu Arg Val Asn Leu Gly Met Asn Val Gly Lys
 675 680 685
 Ala Arg Gly Phe Phe Lys Thr Gly Asp Leu Val Ile Val Leu Thr Gly
 690 695 700
 Trp Arg Pro Gly Ser Gly Tyr Thr Asn Thr Met Arg Val Val Pro Val
 705 710 715 720
 Pro Leu Glu Tyr Pro Tyr Asp Val Pro Asp Tyr Ala His His His His
 725 730 735
 His His

<210> 40

<211> 2217

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 40

atgagaaaaa	aaagaagaca	aagaagaaga	gtggacagcc	tcttgatgaa	ccggaggaag	60
tttctttacc	aattcaaaaa	tgtccgctgg	gctaagggtc	ggcgtgagac	ctacctgtgc	120
tacgtagtga	agaggcgtga	cagtgtctaca	tccttttcac	tggactttgg	ttatcttcgc	180
aataagaacg	gctgccacgt	ggaattgctc	ttcctccgct	acatctcgga	ctgggacctt	240
gaccctggcc	gctgctaccg	cgtcacctgg	ttcacctcct	ggagccoctg	ctacgactgt	300
gcccagacatg	tggccgactt	tctgcgaggg	aaccccaacc	tcagtctgag	gatcttcacc	360
gcgcgcctct	acttctgtga	ggaccgcaag	gctgagcccg	aggggctgcg	gcggctgcac	420
cgcgccgggg	tgcaaatagc	catcatgacc	ttcaaagatt	atctttactg	ctggaatact	480
tttgtagaaa	accatgaaag	aactttcaaa	gcctgggaag	ggctgcatga	aaattcagtt	540

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ogtctctcca gacagcttcg acgaatcctt ttgcccctgt atgaggttga tgacttacga      600
gacgcatttc gtactttggg acttcacgct gccatggcag acacctttct ggagcacatg      660
tgccgcctgg acatcgactc cgagccaacc attgccagaa acaccggcat catetgcacc      720
atcggcccgag cctcccgcctc tgtggacaag ctgaaggaaa tgattaaatc tggaatgaat      780
gttgcccgcgc tcaacttctc gcacggcacc caccgagtac atgagggcac aattaagaac      840
gtgcgagagg ccacagagag ctttgccctc gacccgatca cctacagacc tgtggctatt      900
gcactggaca ccaagggacc tgaatccga actggactca tcaaggggag tggcacagca      960
gaggtggagc tcaagaaggc cgcagctctc aaagtgcgc tggacaatgc cttcatggag     1020
aactgcgatg agaatgtgct gtgggtggac tacaagaacc tcatcaaagt tatagatgtg     1080
ggcagcaaaa tctatgtgga tgacggtctc atttccttgc tggttaagga gaaaggcaag     1140
gactttgtca tgactgaggt tgagaacggt ggcatgcttg gtagtaagaa gggagtgaac     1200
ctcccagggt ctgcggtcga cctgcctgca gtctcagaga aggacattca ggacctgaaa     1260
tttggcgtgg agcagaatgt ggacatgggt ttgcgttctc tcatccgcaa agctgctgat     1320
gtccatgctg tcaggaaggt gctaggggaa aagggaaagc acatcaagat tatcagcaag     1380
attgagaatc acgaggggtg gcgcaggttt gatgagatca tggaggccag cgatggcatt     1440
atggtggccc gtggtgacct ggggtattgag atccctgctg aaaaagtctt cctcgcacag     1500
aagatgatga ttgggcgctg caacagggct ggcaaaccac tcatttgtgc cactcagatg     1560
ttgaaaagca tgatcaagaa acctcgcccg acccgcgctg agggcagtga tgttgccaat     1620
gcagttctgg atggagcaga ctgcatcatg ctgtctgggg agaccgcaa gggagactac     1680
ccactggagg ctgtgcgcat gcagcacgct attgtcgtg aggctgaggc cgcaatgttc     1740
catcgtcagc agtttgaaga aatcttacgc cacagtgtac accacaggga gcctgctgat     1800
gccatggcag caggcgcggt ggaggcctcc ttttaagtgt tagcagcagc tctgatagtt     1860
atgaccgagt ctggcaggtc tgcacacctg gtgtcccgt accgcccgcg ggctcccac     1920
atcgccgtca cccgcaatga ccaaacagca cgccaggcac acctgtaccg cggcgtcttc     1980
cccgtgctgt gcaagcagcc ggcccacgat gcctgggcag aggatgtgga tctcgtgtg     2040
aacctgggca tgaatgtcgg caaagcccgt ggattcttca agaccgggga cctggtgatc     2100
gtgctgacgg gctggcggcc cggctccggc tacaccaaca ccatgcgggt ggtgcccggt     2160
ccactcgagt acccctacga cgtgcccgac tacgccacc accaccacca ccactga      2217

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<210> 41

<211> 530

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 41

```

Met Ser Lys His His Asp Ala Gly Thr Ala Phe Ile Gln Thr Gln Gln
 1           5           10           15
Leu His Ala Ala Met Ala Asp Thr Phe Leu Glu His Met Cys Arg Leu
      20           25           30
Asp Ile Asp Ser Glu Pro Thr Ile Ala Arg Asn Thr Gly Ile Ile Cys
      35           40           45
Thr Ile Gly Pro Ala Ser Arg Ser Val Asp Lys Leu Lys Glu Met Ile
      50           55           60
Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr His
      65           70           75           80
Glu Tyr His Glu Gly Thr Ile Lys Asn Val Arg Glu Ala Thr Glu Ser
      85           90           95
Phe Ala Ser Asp Pro Ile Thr Tyr Arg Pro Val Ala Ile Ala Leu Asp
      100          105          110
Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly Thr
      115          120          125
Ala Glu Val Glu Leu Lys Lys Gly Ala Ala Leu Lys Val Thr Leu Asp

```


130					135					140					
Asn	Ala	Phe	Met	Glu	Asn	Cys	Asp	Glu	Asn	Val	Leu	Trp	Val	Asp	Tyr
145					150				155						160
Lys	Asn	Leu	Ile	Lys	Val	Ile	Asp	Val	Gly	Ser	Lys	Ile	Tyr	Val	Asp
				165					170						175
Asp	Gly	Leu	Ile	Ser	Leu	Leu	Val	Lys	Glu	Lys	Gly	Lys	Asp	Phe	Val
				180					185						190
Met	Thr	Glu	Val	Glu	Asn	Gly	Gly	Met	Leu	Gly	Ser	Lys	Lys	Gly	Val
		195					200					205			
Asn	Leu	Pro	Gly	Ala	Ala	Val	Asp	Leu	Pro	Ala	Val	Ser	Glu	Lys	Asp
		210				215					220				
Ile	Gln	Asp	Leu	Lys	Phe	Gly	Val	Glu	Gln	Asn	Val	Asp	Met	Val	Phe
225					230				235						240
Ala	Ser	Phe	Ile	Arg	Lys	Ala	Ala	Asp	Val	His	Ala	Val	Arg	Lys	Val
				245					250					255	
Leu	Gly	Glu	Lys	Gly	Lys	His	Ile	Lys	Ile	Ile	Ser	Lys	Ile	Glu	Asn
			260					265						270	
His	Glu	Gly	Val	Arg	Arg	Phe	Asp	Glu	Ile	Met	Glu	Ala	Ser	Asp	Gly
		275					280					285			
Ile	Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Ile	Glu	Ile	Pro	Ala	Glu	Lys
		290				295					300				
Val	Phe	Leu	Ala	Gln	Lys	Met	Met	Ile	Gly	Arg	Cys	Asn	Arg	Ala	Gly
305					310				315						320
Lys	Pro	Ile	Ile	Cys	Ala	Thr	Gln	Met	Leu	Glu	Ser	Met	Ile	Lys	Lys
				325					330					335	
Pro	Arg	Pro	Thr	Arg	Ala	Glu	Gly	Ser	Asp	Val	Ala	Asn	Ala	Val	Leu
			340					345					350		
Asp	Gly	Ala	Asp	Cys	Ile	Met	Leu	Ser	Gly	Glu	Thr	Ala	Lys	Gly	Asp
		355					360					365			
Tyr	Pro	Leu	Glu	Ala	Val	Arg	Met	Gln	His	Ala	Ile	Ala	Arg	Glu	Ala
		370				375					380				
Glu	Ala	Ala	Met	Phe	His	Arg	Gln	Gln	Phe	Glu	Glu	Ile	Leu	Arg	His
385					390				395						400
Ser	Val	His	His	Arg	Glu	Pro	Ala	Asp	Ala	Met	Ala	Ala	Gly	Ala	Val
				405					410					415	
Glu	Ala	Ser	Phe	Lys	Cys	Leu	Ala	Ala	Ala	Leu	Ile	Val	Met	Thr	Glu
			420					425					430		
Ser	Gly	Arg	Ser	Ala	His	Leu	Val	Ser	Arg	Tyr	Arg	Pro	Arg	Ala	Pro
		435					440					445			
Ile	Ile	Ala	Val	Thr	Arg	Asn	Asp	Gln	Thr	Ala	Arg	Gln	Ala	His	Leu
		450				455					460				
Tyr	Arg	Gly	Val	Phe	Pro	Val	Leu	Cys	Lys	Gln	Pro	Ala	His	Asp	

17

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<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 42

atgtcgaagc	accacgatgc	agggaccgct	ttcatccaga	cccagcagct	gcacgctgcc	60
atggcagaca	cctttctgga	gcacatgtgc	cgcctggaca	tcgactccga	gccaaccatt	120
gccagaaaca	ccggcatcat	ctgcaccatc	ggcccagcct	cccgtctgtg	ggacaagctg	180
aaggaaatga	ttaaactctgg	aatgaatgtt	gcccgcctca	acttctcgca	cggcaccac	240
gagtatcatg	agggcacaat	taagaacgtg	cgagaggcca	cagagagctt	tgctctgac	300
ccgatcacct	acagacctgt	ggctattgca	ctggacacca	agggacctga	aatccgaact	360
ggactcatca	agggagtgg	cacagcagag	gtggagctca	agaagggcgc	agctctcaaa	420
gtgacgctgg	acaatgcctt	catggagaac	tgcatgaga	atgtgctgtg	ggtggactac	480
aagaacctca	tcaaagttat	agatgtgggc	agcaaaatct	atgtggatga	cggctctcatt	540
tccttgctgg	ttaaggagaa	aggcaaggac	tttgtcatga	ctgagggtga	gaacgggtggc	600
atgcttggtg	gtaagaagg	agtgaacctc	ccagggtgctg	cggctcgacct	gcctgcagtc	660
tcagagaagg	acattcagga	cctgaaatct	ggcgtggagc	agaatgtgga	catggtgttc	720
gcttccttca	tccgcaaagc	tgctgatgtc	catgctgtca	ggaagggtgct	aggggaaaag	780
ggaaagcaca	tcaagattat	cagcaagatt	gagaatcacg	aggggtgtgcg	caggtttgat	840
gagatcatgg	aggccagcga	tggcattatg	gtggcccgctg	gtgacctggg	tattgagatc	900
cctgctgaaa	aagtcttcct	cgcacagaag	atgatgattg	ggcgtctgcaa	cagggtctggc	960
aaacccatca	tttgtgccac	tcagatgttg	gaaagcatga	tcaagaaacc	tcgcccgaacc	1020
cgcgtgaggg	gcagtgatgt	tgccaatgca	gttctggatg	gagcagactg	catcatgctg	1080
tctggggaga	ccgccaagg	agactaccca	ctggaggctg	tgccgatgca	gcacgctatt	1140
gctcgtgagg	ctgaggccgc	aatgttccat	cgtcagcagt	ttgaagaaat	cttacgccac	1200
agtgtacacc	acagggagcc	tgctgatgcc	atggcagcag	gcgcggtgga	ggcctccttt	1260
aagtgccttag	cagcagctct	gatagttatg	accgagctctg	gcagggtctgc	acacctggtg	1320
tcccgggtacc	gcccgcgggc	tcccatcatc	gccgtcaccc	gcaatgacca	aacagcacgc	1380
caggcacacc	tgtaccgcgg	cgtcttcccc	gtgctgtgca	agcagccggc	ccacgatgcc	1440
tgggcagagg	atgtggatct	ccgtgtgaac	ctgggcatga	atgtcgga	agcccgtgga	1500
ttcttcaaga	ccggggacct	ggtgatcgtg	ctgacgggct	ggcgccccgg	ctccggctac	1560
accaacacca	tgcggtggt	gcccggtgcca	tga			1593

<210> 43

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 43

Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg
1					5			

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

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<400> 44
 aqaaaaaaaaa gaagacaaag aagaaga

27

```
<210> 45
<211> 237
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence; note =
        synthetic construct
```

<400>	45																
Met	Thr	Ser	Glu	Lys	Gly	Pro	Ser	Thr	Gly	Asp	Pro	Thr	Leu	Arg	Arg		
1				5					10					15			
Arg	Ile	Glu	Pro	Trp	Glu	Phe	Asp	Val	Phe	Tyr	Asp	Pro	Arg	Glu	Leu		
			20					25					30				
Arg	Lys	Glu	Ala	Cys	Leu	Leu	Tyr	Glu	Ile	Lys	Trp	Gly	Met	Ser	Arg		
		35					40					45					
Lys	Ile	Trp	Arg	Ser	Ser	Gly	Lys	Asn	Thr	Thr	Asn	His	Val	Glu	Val		
	50					55					60						
Asn	Phe	Ile	Lys	Lys	Phe	Thr	Ser	Glu	Arg	Asp	Phe	His	Pro	Ser	Ile		
65					70					75					80		
Ser	Cys	Ser	Ile	Thr	Trp	Phe	Leu	Ser	Trp	Ser	Pro	Cys	Trp	Glu	Cys		
				85					90					95			
Ser	Gln	Ala	Ile	Arg	Glu	Phe	Leu	Ser	Arg	His	Pro	Gly	Val	Thr	Leu		
			100					105					110				
Val	Ile	Leu	Tyr	Val	Ala	Arg	Leu	Phe	Trp	His	Met	Asp	Gln	Gln	Asn		
	115						120					125					
Arg	Gln	Gly	Leu	Arg	Asp	Leu	Val	Asn	Ser	Gly	Val	Thr	Ile	Gln	Ile		
	130					135					140						
Met	Arg	Ala	Ser	Glu	Tyr	Tyr	His	Cys	Trp	Arg	Asn	Phe	Val	Asn	Tyr		
145				150					155					160			
Pro	Pro	Gly	Asp	Glu	Ala	His	Trp	Pro	Gln	Tyr	Pro	Pro	Leu	Trp	Met		
				165					170					175			
Met	Leu	Tyr	Ala	Leu	Glu	Leu	His	Cys	Ile	Ile	Leu	Ser	Leu	Pro	Pro		
			180					185					190				
Cys	Leu	Lys	Ile	Ser	Arg	Arg	Trp	Gln	Asn	His	Leu	Thr	Phe	Phe	Arg		
		195					200					205					
Leu	His	Leu	Gln	Asn	Cys	His	Tyr	Gln	Thr	Ile	Pro	Pro	His	Ile	Leu		
	210					215					220						
Leu	Ala	Thr	Gly	Leu	Ile	His	Pro	Ser	Val	Ala	Trp	Arg					
225					230					235							

```
<210> 46
<211> 9
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence; note =
        synthetic construct
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<400> 46
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

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<210> 47
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 47
 taccctacg acgtgccgga ctacgcc

27

<210> 48
 <211> 429
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 48
 Met Gly Pro Phe Cys Leu Gly Cys Ser His Arg Lys Cys Tyr Ser Pro
 1 5 10 15
 Ile Arg Asn Leu Ile Ser Gln Glu Thr Phe Lys Phe His Phe Lys Asn
 20 25 30
 Leu Arg Tyr Ala Ile Asp Arg Lys Asp Thr Phe Leu Cys Tyr Glu Val
 35 40 45
 Thr Arg Lys Asp Cys Asp Ser Pro Val Ser Leu His His Gly Val Phe
 50 55 60
 Lys Asn Lys Asp Asn Ile His Ala Glu Ile Cys Phe Leu Tyr Trp Phe
 65 70 75 80
 His Asp Lys Val Leu Lys Val Leu Ser Pro Arg Glu Glu Phe Lys Ile
 85 90 95
 Thr Trp Tyr Met Ser Trp Ser Pro Cys Phe Glu Cys Ala Glu Gln Val
 100 105 110
 Leu Arg Phe Leu Ala Thr His His Asn Leu Ser Leu Asp Ile Phe Ser
 115 120 125
 Ser Arg Leu Tyr Asn Ile Arg Asp Pro Glu Asn Gln Gln Asn Leu Cys
 130 135 140
 Arg Leu Val Gln Glu Gly Ala Gln Val Ala Ala Met Asp Leu Tyr Glu
 145 150 155 160
 Phe Lys Lys Cys Trp Lys Lys Phe Val Asp Asn Gly Gly Arg Arg Phe
 165 170 175
 Arg Pro Trp Lys Lys Leu Leu Thr Asn Phe Arg Tyr Gln Asp Ser Lys
 180 185 190
 Leu Gln Glu Ile Leu Arg Pro Cys Tyr Ile Pro Val Pro Ser Ser Ser
 195 200 205
 Ser Ser Thr Leu Ser Asn Ile Cys Leu Thr Lys Gly Leu Pro Glu Thr
 210 215 220
 Arg Phe Cys Val Glu Gly Arg Arg Val His Leu Leu Ser Glu Glu Glu
 225 230 235 240
 Phe Tyr Ser Gln Phe Tyr Asn Gln Arg Val Lys His Leu Cys Tyr Tyr
 245 250 255

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His Gly Met Lys Pro Tyr Leu Cys Tyr Gln Leu Glu Gln Phe Asn Gly
 260 265 270
 Gln Ala Pro Leu Lys Gly Cys Leu Leu Ser Glu Lys Gly Lys Gln His
 275 280 285
 Ala Glu Ile Leu Phe Leu Asp Lys Ile Arg Ser Met Glu Leu Ser Gln
 290 295 300
 Val Ile Ile Thr Cys Tyr Leu Thr Trp Ser Pro Cys Pro Asn Cys Ala
 305 310 315 320
 Trp Gln Leu Ala Ala Phe Lys Arg Asp Arg Pro Asp Leu Ile Leu His
 325 330 335
 Ile Tyr Thr Ser Arg Leu Tyr Phe His Trp Lys Arg Pro Phe Gln Lys
 340 345 350
 Gly Leu Cys Ser Leu Trp Gln Ser Gly Ile Leu Val Asp Val Met Asp
 355 360 365
 Leu Pro Gln Phe Thr Asp Cys Trp Thr Asn Phe Val Asn Pro Lys Arg
 370 375 380
 Pro Phe Trp Pro Trp Lys Gly Leu Glu Ile Ile Ser Arg Arg Thr Gln
 385 390 395 400
 Arg Arg Leu His Arg Ile Lys Glu Ser Trp Gly Leu Gln Asp Leu Val
 405 410 415
 Asn Asp Phe Gly Asn Leu Gln Leu Gly Pro Pro Met Ser
 420 425

<210> 49

<211> 1948

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 49

acttggcccg	ggaggtcagt	ttcacttctg	ggggcttctc	atagcctgct	cacagaaaat	60
gcaaccccg	cgcattgggc	ccagagctgg	gatgggacca	ttctgtctgg	gatgcagcca	120
tcgcaaatgc	tattcaccga	tcagaaacct	gatattctca	gaaacattca	aattccactt	180
taagaacct	cgctatgcc	tagaccggaa	agataccttc	ttgtgctatg	aagtgcactg	240
aaaggactgc	gattcaccgc	tctcccttca	ccatgggggtc	tttaagaaca	aggacaacat	300
ccacgctgaa	atctgctttt	tatactgggt	ccatgacaaa	gtactgaaag	tgctgtctcc	360
gagagaagag	ttcaagatca	cctggatat	gtcctggagc	ccctgtttcg	aatgtgcaga	420
gcaggtacta	aggttcctgg	ctacacacca	caacctgagc	ctggacatct	tcagctcccg	480
cctctacaac	atacggggacc	cagaaaacca	gcagaatctt	tgaggctgg	ttcaggaagg	540
agcccagggtg	gctgoccatg	acctatacga	atttaaaaag	tggtggaaga	agtttgtgga	600
caatggcggc	aggcgattca	ggccttggaa	aaaactgctt	acaaatttta	gataccagga	660
ttctaagctt	caggagattc	tgagaccttg	ctacatcccg	gtcccttcca	gctcttcac	720
cactctgtca	aatatctgtc	taacaaaagg	tctcccagag	acgaggttct	gcgtggaggg	780
caggcgagtg	cacctgctaa	gtgaagagga	attttactcg	cagttttaca	accaacgagt	840
caagcatctc	tgctactacc	acggcatgaa	gccctatcta	tgctaccagc	tggagcagtt	900
caatggccaa	gogccactca	aaggctgcct	gctaagcgag	aaaggcaaac	agcatgcaga	960
aatcctcttc	cttgataaga	ttcgggtccat	ggagctgagc	caagtgataa	tcacctgcta	1020
cctcacctgg	agcccctgcc	caaactgtgc	ctggcaactg	gcggcattca	aaaggatcg	1080
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